

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/022,390A

Source: 1Fw/6

Date Processed by STIC: 1/10/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/022,390A

TIME: 14:30:41

Input Set : E:\912SEQ.002.txt

Output Set: N:\CRF4\01102006\J022390A.raw

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3 <110> APPLICANT: Vega, Manuel
4      Drittanti, Lila
5      Flaux, Marjorie
7 <120> TITLE OF INVENTION: MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES
9 <130> FILE REFERENCE: 37851-912
11 <140> CURRENT APPLICATION NUMBER: 10/022,390A
12 <141> CURRENT FILING DATE: 2001-12-17
14 <150> PRIOR APPLICATION NUMBER: 60/315,382
15 <151> PRIOR FILING DATE: 2001-08-27
18 <160> NUMBER OF SEQ ID NOS: 749
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 621
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Mutant rep protein: rep78 4 GCT
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32 1          5          10          15
33 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
34          20          25          30
35 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
36          35          40          45
37 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
38          50          55          60
39 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
40 65          70          75          80
41 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
42          85          90          95
43 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
44          100         105         110
45 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
46          115         120         125
47 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
48          130         135         140
49 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
50 145         150         155         160
51 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
52          165         170         175
53 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
54          180         185         190
55 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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57 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
58      210          215          220
59 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
60 225          230          235          240
61 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
62          245          250          255
63 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
64          260          265          270
65 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
66          275          280          285
67 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
68          290          295          300
69 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
70 305          310          315          320
71 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
72          325          330          335
73 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
74          340          345          350
75 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
76          355          360          365
77 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
78          370          375          380
79 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
80 385          390          395          400
81 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
82          405          410          415
83 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
84          420          425          430
85 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
86          435          440          445
87 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
88          450          455          460
89 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
90 465          470          475          480
91 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
92          485          490          495
93 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
94          500          505          510
95 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
96          515          520          525
97 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
98          530          535          540
99 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
100 545          550          555          560
101 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
102          565          570          575
103 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
104          580          585          590

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105 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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107 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
108           610                      615                      620
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 536
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Mutant rep protein: rep68 4 GCT
118 <400> SEQUENCE: 2
119 Thr Ala Gly Ala Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
120   1           5           10           15
121 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
122           20           25           30
123 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
124           35           40           45
125 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
126           50           55           60
127 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
128 65           70           75           80
129 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
130           85           90           95
131 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
132           100          105          110
133 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
134           115          120          125
135 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
136           130          135          140
137 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
138 145          150          155          160
139 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
140           165          170          175
141 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
142           180          185          190
143 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
144           195          200          205
145 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
146           210          215          220
147 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
148 225          230          235          240
149 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
150           245          250          255
151 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
152           260          265          270
153 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
154           275          280          285
155 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
156           290          295          300

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Input Set : E:\912SEQ.002.txt

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157 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
158 305          310          315          320
159 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
160          325          330          335
161 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
162          340          345          350
163 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
164          355          360          365
165 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
166          370          375          380
167 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
168 385          390          395          400
169 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
170          405          410          415
171 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
172          420          425          430
173 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
174          435          440          445
175 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
176          450          455          460
177 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
178 465          470          475          480
179 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
180          485          490          495
181 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
182          500          505          510
183 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
184          515          520          525
185 Arg Leu Ala Arg Gly His Ser Leu
186          530          535
188 <210> SEQ ID NO: 3
189 <211> LENGTH: 621
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Mutant rep protein: rep78 10 GCG
196 <400> SEQUENCE: 3
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198 1          5          10          15
199 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
200          20          25          30
201 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
202          35          40          45
203 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
204          50          55          60
205 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
206 65          70          75          80
207 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
208          85          90          95

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Input Set : E:\912SEQ.002.txt

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209 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
210      100      105      110
211 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
212      115      120      125
213 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
214      130      135      140
215 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
216 145      150      155      160
217 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
218      165      170      175
219 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
220      180      185      190
221 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
222      195      200      205
223 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
224      210      215      220
225 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
226 225      230      235      240
227 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
228      245      250      255
229 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
230      260      265      270
231 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
232      275      280      285
233 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
234      290      295      300
235 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
236 305      310      315      320
237 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
238      325      330      335
239 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
240      340      345      350
241 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
242      355      360      365
243 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
244      370      375      380
245 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
246 385      390      395      400
247 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
248      405      410      415
249 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
250      420      425      430
251 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
252      435      440      445
253 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
254      450      455      460
255 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
256 465      470      475      480
257 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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**VERIFICATION SUMMARY**

DATE: 01/10/2006

PATENT APPLICATION: US/10/022,390A

TIME: 14:30:42

Input Set : E:\912SEQ.002.txt

Output Set: N:\CRF4\01102006\J022390A.raw